

1 tttaggtgac actatagaat actcaagctt gactaaatat ttagaaaagca catttgtgtc  
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 121 aattgcctca agggaaagcat acaatgaata agttattttg gtacttcctc aaaatagcca  
 181 acacaatagg gaaatggaga aaatgtactc tgaacacccat gaaaaggga cctgaaaatc  
 241 taatgtgtaa acttggagaa atgacattag aaaacgaaag ctacaaaaga gaacactctt  
 301 caaaataatc tgagatgcat gaaaggcaaa cattcactag agctggaatt tccctaagtc  
 361 tatgcaggga taagtagcat atttgacctt caccatgatt atcaagcact tctttggaac  
 421 tgtgttgggt ctgctggcct ctaccactat cttctctcta gatttgaac tgattatctt  
 481 ccagcaaaga caagtgaatc aagaaagtctt aaaactcttg aataagttgc aaaccttgtc  
 541 aattcagcag tgtctaccac acaggaaaaa cttctctgctt cctcagaagt ctttgagtcc  
 601 tcagcagtac caaaaaggac acactctggc cattctccat gagatgcttc agcagatctt  
 661 cagcctcttc agggcaataa tttctctgga tggttgggag gaaaaccaca cggagaattt  
 721 cctcattcaa ctctcatcaac agctagaata cctagaagca ctcatgggac tgggaagcaga  
 781 gaagctaagt ggtactttgg gtagtgataa ccttagatta caagttaaaa tgtacttccg  
 841 aaggatccat gattacctgg aaaaccagga ctacagcacc tgtgcctggg ccattgtcca  
 901 agtagaaaac agccgatgct tgttctttgt gttcagtcct acagaaaaac tgagcaaaca  
 961 aggaagacct ttgaacgaca tgaagcaaga gcttactaca gagtttagaa gcccgaggta  
 1021 ggtggaggga ctagaggact tctccagaca tgattcttca tagagtggta atacaattta  
 1081 tagtacaatc acattgtctt gattttgtgt atatatatat tatctgtgt ttttaagattg  
 1141 tgcatattga ccacaattgt ttttattttg taatgtggct ttatatattc tatccatttt  
 1201 a

Figure 1

MIKHFFGTVLVLLASTTIFSLDKLIIFQQRQVNQESLKLLNKLQTL~~SIQQCLPH~~  
RKNFLLPQKSLS~~PQQYQK~~GHTLAILHEMLQQIFSLFRANISLDGWEE~~NHTEK~~  
FLIQLHQQLEYLEALMGLEAEKLSGTLGSDNLR~~LQVKMYFRRIHDY~~LENQD  
YSTCAWAIVQVEISRCLFFVFSLTEKLSKQGRPLNDMKQELTTEFRSPR

Figure 2

0984050-11301

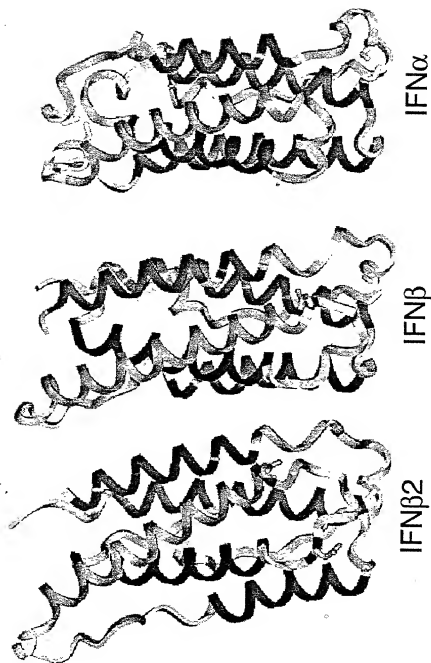
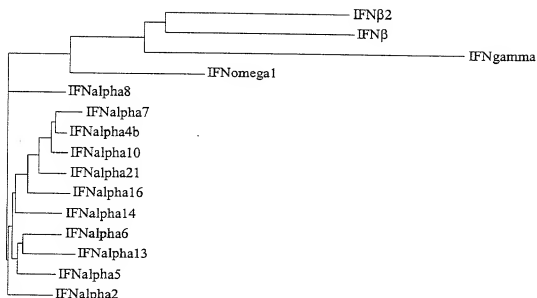


Figure 3

	1		70
IFNB2	(1)	MILKHHFGTVLVLLASTIPFSLDLKLIIFQORQVNOESLKLNLKIQ-TESIQOCLPHRKNFLLPQKSLSP	
IFNB	(1)	MTNKKLQETALLICFSTIALMSYNNLGLQRSSNFQCKLLWQNLGRLEY---CLKDRMNFDPBETIKQL	
IFNAlpha8	(1)	MALTFFYLLVALVVLVSYSKSFSLGCDLPQTHS-LGNRRATILLAQMR-RISPFSCCLKDRHDFGFPQEEFDD	
IFNAlpha7	(1)	MARSFSLMLVVLVLSYKSCISLGCGLPQTHS-LNRRALILLAQMGR-RISPFSCCLKDRHDFGFPQEEFDD	
IFNAlpha6	(1)	MALFPALLMALVVLVLSKSSCSLGCGLPQTHS-LGHRRTMLMLAQMR-RISLFSCLKDRHDFGFPQEEFDD	
IFNAlpha5	(1)	MALFPVLLMALVVLVLSKSCISLGCGLPQTHS-LNRRALILLAQMGR-RISPFSCCLKDRHDFGFPQEEFDD	
IFNAlpha4b	(1)	MALSFSLMALVVLVLSYKSCISLGCGLPQTHS-LGNRRATILLAQMR-RISHTFSCCLKDRHDFGFPQEEFDD	
IFNAlpha21	(1)	MALSFSLMALVVLVLSYKSCISLGCGLPQTHS-LGNRRALILLAQMGR-RISPFSCCLKDRHDFGFPQEEFDD	
IFNAlpha2	(1)	MALTFFYLLVALVVLVSCKSSCSVGCGLPQTHS-LGSRRTMLMLAQMR-RISLFSCLKDRHDFGFPQEEFDD	
IFNAlpha16	(1)	MALSFSLMALVVLVLSYKSCISLGCGLPQTHS-LGNRRATILLAQMR-RISHTFSCCLKDRHDFGFPQEEFDD	
IFNAlpha14	(1)	MALFPALLMALVVLVLSKSSCSLGCGLPQTHS-LGNRRATILLAQMR-RISHTFSCCLKDRHDFGFPQEEFDD	
IFNAlpha13	(1)	MALFPALLMALVVLVLSKSSCSLGCGLPQTHS-LNRRRTMLMLAQMR-RISPFSCCLKDRHDFGFPQEEFDD	
IFNAlpha10	(1)	MALSFSLMALVVLVLSYKSCISLGCGLPQTHS-LGNRRALILLAQMGR-RISPFSCCLKDRHDFGFPQEEFDD	
IFNomega1	(1)	MALFPALLMALVMTSPVSGSLGCGLPQNHG-LLSRNTLVLLHQMGR-RISFELCLKDRHDFGFPQEEFDD	
IFNgamma	(1)	MKYT-SYLLAFQFCIVGLSGCYCQDEYVKE----AENLKKYFNAG----H--SDVADNGTLF--LGLLK	
Consensus	(1)	MAL F LLMALLVLS KS CSLGCDLPQTHS L NRR L LLAQM RISPFSCCLKDRHDF FPQEEFDD	
	71		140
IFNB2	(70)	QOYQKHTLALHLEMQQIFSLFRANISLDGHEENHTKEFLIQLHOOLEYLEALMGLAEKLSGTIGSDN	
IFNB	(69)	QOQKEDAAITVEMLIQNFATFRQDSSSTGWNETIIVENMLANVHQINHLKTVLEEKTEKEDFTRGKML	
IFNAlpha8	(69)	QOQKAQAIISVLHEMIQQTFLNLFSTKDSSAALDETLLEDFYIELDQQLNDLESCVMQEVGVIESPLMYED	
IFNAlpha7	(69)	HQFQKTQAIISVLHEMIQQTFLNLFSTEDSSAAWQSLLEKFEETELYQQLNDLEACVIOEVGVETPLMNE	
IFNAlpha6	(69)	NQFQKAEAIISVLHEVIQQTFLNLFSTKDSSAANDERLLDKFYTELQQLNDLEACVIOEVGVETPLMNE	
IFNAlpha5	(69)	NQFQKAQAIISVLHEMIQQTFLNLFSTKDSSATWDETLLDKFYTELQQLNDLEACVMQEVGVETPLMNV	
IFNAlpha4b	(69)	HQFQKTQAIISVLHEMIQQTFLNLFSTEDSSAAWQSLLEKFEETELYQQLNDLEACVIOEVGVETPLMNV	
IFNAlpha21	(69)	NQFQKAQAIISVLHEMIQQTFLNLFSTKDSSATWQSLLEKFEETELYQQLNDLEACVIOEVGVETPLMNV	
IFNAlpha2	(69)	NQFQKAETIPVLHEMIQQTFLNLFSTKDSSAANDETLLDKFYTELQQLNDLEACVIOEVGVETPLMNE	
IFNAlpha16	(69)	NQFQKAQAIISAFHEMIQQTFLNLFSTKDSSAANDETLLDKFYTELQQLNDLEACVIOEVGVETPLMNE	
IFNAlpha14	(69)	NQFQKAQAIISVLHEMIQQTFLNLFSTKSSAANDETLLDKFYTELQQLNDLEACVIOEVGVETPLMNE	
IFNAlpha13	(69)	NQFQKAPAIISVLHELIQQTFLNLFSTKDSSAANDETLLDKFYTELQQLNDLEACVIOEVGVETPLMNE	
IFNAlpha10	(69)	NQFQKAQAIISVLHEMIQQTFLNLFSTEDSSAAWQSLLEKFEETELYQQLNDLEACVIOEVGVETPLMNE	
IFNomega1	(69)	SOLQKAHVMSVLHEMIQQTFLNLFSTKSSAANDETLLDKFYTELQQLNDLEACVMQEBRGVETPLMNE	
IFNgamma	(58)	NWKEBSDRKIMQSOIVSYFPYKLPKFNFKD---DOS-KQSVETIKEDIN-VKFFNSNKKKIVDFEKITNY	
Consensus	(71)	NQFQKAQAIISVLHEMIQQTFLNLFSTKDSSAAND LLDKF TELYQQLNDLEACV QEVGVETPLMN D	
	141		210
IFNB2	(140)	LRLOVKMYFRRIHDYLE-NQDYSTCAWATVQVEISRCFLFFVSLTEKLSKOGRPNDMKQELTEFRSPR	
IFNB	(139)	SSLHKKRYGRIILHYLK-AKEYSHCAWITVRVEILRNVEYINRLTGVLRN---	
IFNAlpha8	(139)	SILAVRKYFORITLYLT-EKKYSPCAWEVVRAEIMRSFSLSNLQKRLRKE---	
IFNAlpha7	(139)	FILAVRKYFORITLYLM-EKKYSPCAWEVVRAEIMRSFSGFSTNLQKRLRKE---	
IFNAlpha6	(139)	SILAVRKYFORITLYLT-EKKYSPCAWEVVRAEIMRSFSLSNLQKRLRKE---	
IFNAlpha5	(139)	SILAVRKYFORITLYLT-EKKYSPCAWEVVRAEIMRSFSLSNLQKRLRKE---	
IFNAlpha4b	(139)	SILAVRKYFORITLYLT-EKKYSPCAWEVVRAEIMRSFSLSNLQKRLRKE---	
IFNAlpha21	(139)	SILAVRKYFORITLYLT-EKKYSPCAWEVVRAEIMRSFSLSNLQKRLRKE---	
IFNAlpha2	(139)	SILAVRKYFORITLYLK-EKKYSPCAWEVVRAEIMRSFSLSNLQKRLRKE---	
IFNAlpha16	(139)	SILAVRKYFORITLYLM-EKKYSPCAWEVVRAEIMRSFSGFSTNLQKRLRKE---	
IFNAlpha14	(139)	SILAVRKYFORITLYLM-EKKYSPCAWEVVRAEIMRSFSGFSTNLQKRLRKE---	
IFNAlpha13	(139)	SILAVRKYFRITLYLT-EKKYSPCAWEVVRAEIMRSLSLSTNLQKRLRKE---	
IFNAlpha10	(139)	SILAVRKYFORITLYLI-EKKYSPCAWEVVRAEIMRSLSFSTNLQKRLRKE---	
IFNomega1	(139)	PALTIREYFOGIRVYLK-EKKYSDCAWEVVRMEIMRSFLSTNLQKRLRKE---	
IFNgamma	(122)	SVTDNLVQRKAHETIQVMAELSGAGTKVR---KRSQML---FAGTRAGQ---	
Consensus	(141)	SILAVRKYFORITLYL EKKYSPCAWEVVRAEIMRSFS STNLQ RLRRK	

Figure 4

# Protein Level Comparison



# Nucleotide Level Comparison

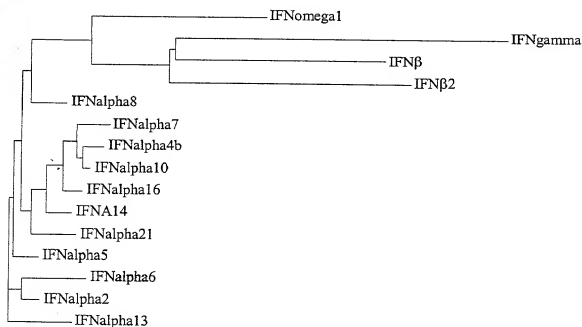
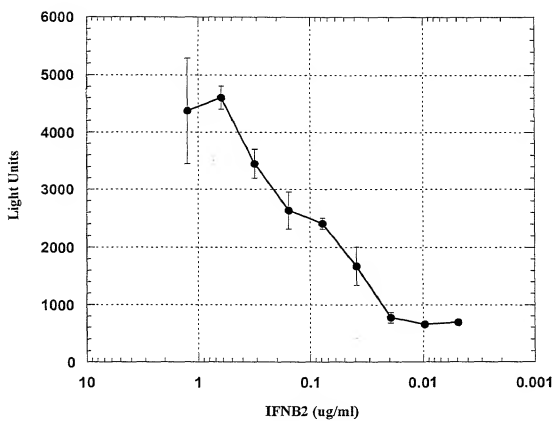


Figure 5

**Figure 6**

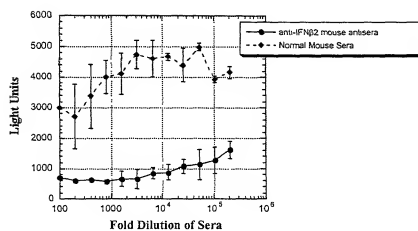
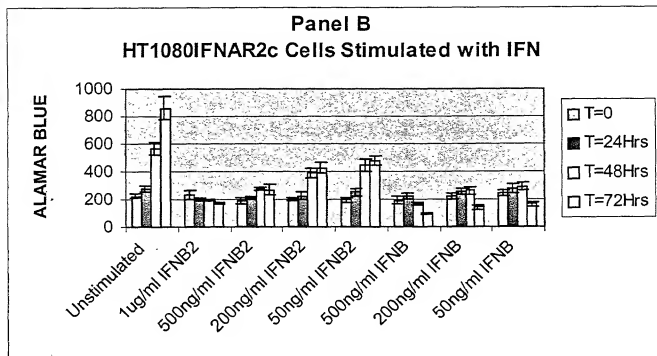
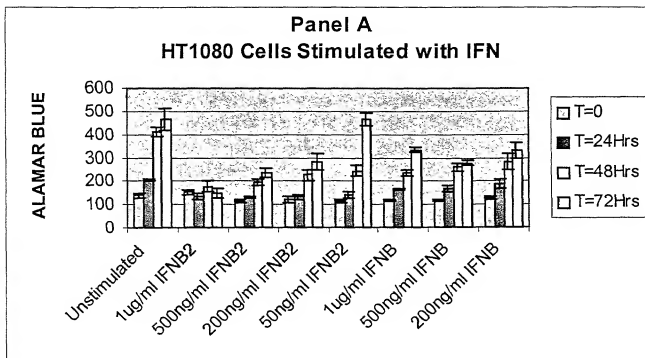
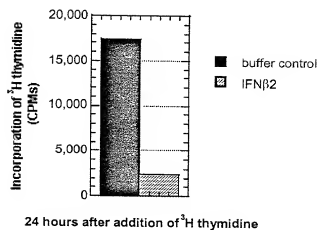


Figure 7

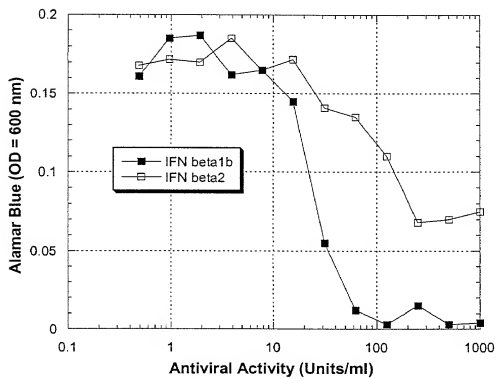
09881050-111301

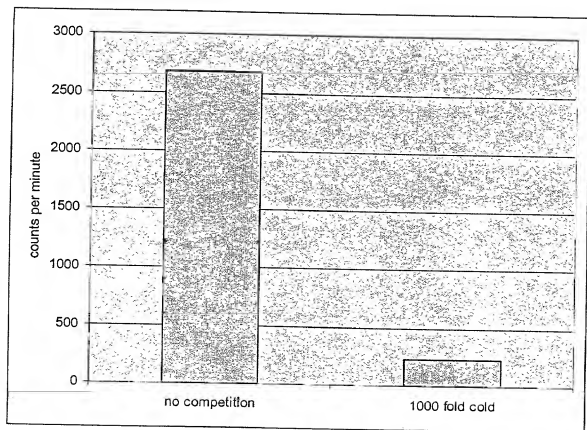


**Figure 8**



**Figure 9**

**Figure 10**



**Figure 11**

1    tttagggtgac actatagaat actcaagcct gactaaaatat ttagaaaagca cattgtgttc  
 61    agtgaaactt tgtatataat gaatagaata ataaaaagatt atgttggatg actagtctgt  
 121   aattgcctca aggaaagcat acaatgaata agttattttg gtacttcctc aaaatagcca  
 181   acacaatagg gaaatggaga aaatgtactc tgaacacccat gaaaagggaa cctgaaaatc  
 241   taatgtgtaa acttggagaa atgacattag aaaacgaaag ctacaaaaga gaacactctt  
 301   caaaataatc tgagatgcat gaaaggcaaa cattcactag agctggaatt tcctaagtc  
 361   tatgcaggga taagtagcat atttgacctt cacc

Figure 12

09881050-111301

361 atgatt atcaagcact tctttggaac  
421 tgtgttggtg ctgctggcct ctaccactat cttctctcta gatttgaac tgattatctt  
481 ccagcaaaga caagtgaatc aagaaagttt aaaactcttg aataagttgc aaaccttgtc  
541 aattcagcag tgtctaccac acaggaaaaa ctttctgctt cctcagaagt ctttgagtcc  
601 ttaactgtac caaaaaggac acactctggc cattcttcat gagatgct

Figure 13

09881050.11301

MIKHFFGTVLVLLASTTIFSLDLKLIHFQQRQVNQESLKLLNKLQTLISQ  
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Figure 14

09881050.111301

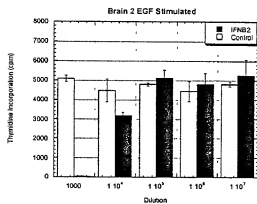
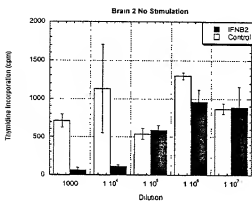
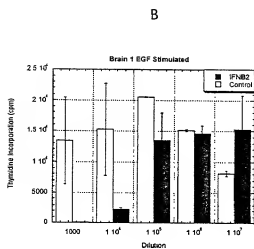
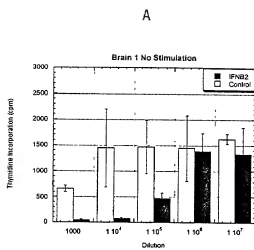


Figure 15